RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/542,867
Source: Pyr
Date Processed by STIC: 2/2/06

ENTERED

PCT

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        RAW SEQUENCE LISTING              DATE: 02/02/2006
        PATENT APPLICATION:  US/10/542,867   TIME: 11:41:17

        Input Set : E:\401uspc.app.txt
        Output Set: N:\CRF4\02022006\J542867.raw
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 3 <110> APPLICANT: Shinoda, Tetsuro
 4        Itoyama, Kyo
 5        Hamamura, Tetsuzo
 8 <120> TITLE OF INVENTION: JUVENILE HORMONE ACID METHYLTRANSFERASE
 9        GENES AND METHODS OF USING SAME
11 <130> FILE REFERENCE: 480230.401USPC
13 <140> CURRENT APPLICATION NUMBER: US 10/542,867
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C--> 14 <141> **CURRENT FILING DATE**: 2005-07-20

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16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00415
17 <151> PRIOR FILING DATE: 2003-01-20
19 <160> NUMBER OF SEQ ID NOS: 38
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2890
25 <212> TYPE: DNA
26 <213> ORGANISM: Bombyx mori
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (125)..(961)
31 <223> OTHER INFORMATION:
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36 tacgaactta aaaaaaaaaa gtgccgacaa atattttatt gcaaaaaaaa atattaagtc     120
38 aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag     169
39      Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys
40      1               5                   10                  15
42 aga gat gct ctg cgc tgc ctc gag gaa cat gcg aat aag att aag tgg     217
43 Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp
44              20                  25                  30
46 aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt     265
47 Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser
48              35                  40                  45
50 gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta     313
51 Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu
52          50                  55                  60
54 gtt ggc tgc gac ata agc gaa gaa atg gtg aaa tac gcg aat aaa cac     361
55 Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His
56      65                  70                  75
58 cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat     409
59 His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp
60 80                  85                  90                  95
62 ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac     457
63 Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr
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Input Set : E:\401uspc.app.txt
Output Set: N:\CRF4\02022006\J542867.raw

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64                100               105               110
66 acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc      505
67 Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe
68                115               120               125
70 aat ctg ctt ggc gac gaa gga gat tgc tta ctt ctg ttc ctg ggc cac      553
71 Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His
72                130               135               140
74 act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg      601
75 Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp
76    145               150               155
78 cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac      649
79 His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp
80 160               165               170               175
82 aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga      697
83 Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly
84                180               185               190
86 ttt agc aat att gaa gtg caa tgc aaa acg ttg ttc tat gta tac gat      745
87 Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp
88                195               200               205
90 gat ttg gat gtt tta aaa aaa tca gta gca gct atc aat cca ttt aat      793
91 Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn
92    210               215               220
94 atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta      841
95 Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val
96    225               230               235
98 gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa      889
99 Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu
100 240               245               250               255
102 tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga     937
103 Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg
104                260               265               270
106 aaa tta tgt tta agt tta atg taa ttaagttaga aaaaaaaac aaatccgact     991
107 Lys Leu Cys Leu Ser Leu Met
108                275
110 tctaaatctt ggaaataagt tttttttaaca tatttctctc tctttgtctt cccagatttt  1051
112 cgtgattaag ctttctattc actattttaa aaagctttct caatatattg aatacagttt  1111
114 agaatacagt tggtatctga aatcactgat ttcgaagtcg gttacttaga acaaatttaa  1171
116 ttagttaatt gtatttataa ggaacgctac aatatttatt acagtaagta attttaaatt  1231
118 tccggaaaca gtggagttca gtggacaatg cagtatcagg agatggctta gatggatgga  1291
120 cgagctcaca gtcacccggt gttaagtggt tactggagcc catagacatc tacaatgtaa  1351
122 atgccgccac cgatatgagt tataaggtct cagaatagct gccccaccct tcaagccgaa  1411
124 acgcgttact gcttcacggc agaaataggc agggcggtgg tacctacccg cgcggactta  1471
126 caagagctcc taccactagt gagagccagc tgcttttgt tgtcgtgtaa aatcggtcgt   1531
128 tgtctctagt catatcatag ccgtacaaaa aaatagacaa cttgatatta taactgttct  1591
130 tcaaatttct cgtcacacat acgaaaataa agtttgatgt atttacccga aatataaatg  1651
132 ttaacatagc tcatacatac atacatatat aattcatata tacacattaa gttttaatac  1711
134 tctgaaatat gtctacccca aaacaagaaa gcctactgta ctaaaattgt atgcagtttt  1771
136 agttttaatg tattatttta ataacagtga catctattag cgatacattg aactatttca  1831
138 acacaacatt tttcatatta ttttcctttg aatctaatta cttttttaa gccgcagtaa   1891
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140 gatggcggtg ttgtacgact taaagtgttg agaatttaaa ataatttcta cggttgttaa   1951
142 attataattg aaatagaaat ccatactatt ttaattactc aactcaacaa ctcaattatt   2011
144 ttttaaagga gatgtgtgag tgagcatcac tagagaattg tttgaccgtt gaccgattgg   2071
146 gctgatttct ttttcattat atccgtaaat tttaggacaa gttttgtacc accaactaca   2131
148 gccactacag tattcattga tttttaatta ccataagttt ggtttgtgta aagtatattt   2191
150 ataataacga taaatttggt ttgagtcgtg atagttggac atttcaacta gtccgcttgc   2251
152 tcatttgatt atactatgtg cttagtgcgg gttcttttac gctatcgaga acgttaaaga   2311
154 actcgcacta agcacactat tgtattttat ttgttgcaca aatatattta gaaacaatcg   2371
156 tgtataatca tcatgcttta aaagtattcc tataaaatca taaacagtca caaaatttat   2431
158 ttttagtgag aattacatga aacaaattat gaaacaaagt ttgattatac tttcaaatgt   2491
160 ttcattactg tttttaagct taaggtataa aatggcatgt ttgtgtgttt actcaggccc   2551
162 taagcaacac gcgttggctt ttaagtaaac tttgaagtct tagttattcc tgggtttatt   2611
164 tggcacgtta gtaaaatcta ccctgccatt tagtaccatt agagtgcgaa tgattacagc   2671
166 gtatgattat tgtttacatt tttaattttt gttaattact taacgaaacc tgcccgggat   2731
168 ttattgacaa cataattagt aaaacatgtg ataatttgaa caatgacaaa tttattgtta   2791
170 gttaatttat ttcactttgt atataataat tgtaagtgtg atgtttaaat aaataaaact   2851
172 aaagtgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa                           2890
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 278
177 <212> TYPE: PRT
178 <213> ORGANISM: Bombyx mori
180 <400> SEQUENCE: 2
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185             20                  25                  30
187 Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val
188         35                  40                  45
190 Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val
191     50                  55                  60
193 Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
194 65                  70                  75                  80
196 Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
197             85                  90                  95
199 Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
200             100                 105                 110
202 Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
203         115                 120                 125
205 Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
206     130                 135                 140
208 Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
209 145                 150                 155                 160
211 Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
212             165                 170                 175
214 Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
215             180                 185                 190
217 Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp
218         195                 200                 205
220 Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile
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221     210                    215                   220
223 Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val
224 225                    230                235                   240
226 Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser
227                    245                250                   255
229 Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg Lys
230                    260                265                   270
232 Leu Cys Leu Ser Leu Met
233          275
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 938
238 <212> TYPE: DNA
239 <213> ORGANISM: Drosophila melanogaster
241 <220> FEATURE:
242 <221> NAME/KEY: CDS
243 <222> LOCATION: (1)..(894)
244 <223> OTHER INFORMATION:
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251 gat gcc aaa ttg att ctg gat gag ttc gca tcg acc atg cag tgg cga    96
252 Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
253          20                  25                  30
255 tcc gat gga gag gat gcc ctc ctg gat gtg ggt tca gga tct ggt aac   144
256 Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
257          35                  40                  45
259 gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg   192
260 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
261      50                  55                  60
263 gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat   240
264 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
265 65                  70                  75                  80
267 tac cag cga gag gag cgt acc aga ttc cag gtt ctg gac att gga tgc   288
268 Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
269                    85                  90                  95
271 gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg   336
272 Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
273          100                 105                 110
275 ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat   384
276 Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
277          115                 120                 125
279 atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt   432
280 Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
281      130                 135                 140
283 ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat   480
284 Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
285 145                 150                 155                 160
287 gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca   528
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288 Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
289             165             170             175
291 ctt cac tac agt cta aat cct ggc gag gaa ttc agc cag ttg ttg aac       576
292 Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
293             180             185             190
295 gat gtg ggt ttc gtg caa cac aat gtg gaa att cga aac gaa gtg ttt       624
296 Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
297         195             200             205
299 gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt       672
300 Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
301         210             215             220
303 cct ttt ctt gag cga atg cct gca gat ttg cat gaa cag ttc ctg gat       720
304 Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
305 225             230             235             240
307 gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat       768
308 Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
309             245             250             255
311 aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat       816
312 Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
313             260             265             270
315 gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca       864
316 Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
317             275             280             285
319 cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca         914
320 His Gln Asn Leu Val Lys Gly Ile Asn
321         290                 295
323 gtaattgcat ttgttaacag agtc                                            938
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 297
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 4
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335 Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
336             20              25              30
338 Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
339         35              40              45
341 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
342     50              55              60
344 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
345 65              70              75              80
347 Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
348             85              90              95
350 Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
351             100             105             110
353 Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
354             115             120             125
356 Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/02/2006
PATENT APPLICATION: **US/10/542,867**   TIME: 11:41:18

Input Set : **E:\401uspc.app.txt**
Output Set: **N:\CRF4\02022006\J542867.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 6,15
Seq#:20; N Pos. 6,12
Seq#:29; Xaa Pos. 2,3,5,7
Seq#:30; Xaa Pos. 5,8,9,13
Seq#:31; Xaa Pos. 1,4
Seq#:32; Xaa Pos. 1,3,10
Seq#:33; Xaa Pos. 9
Seq#:34; Xaa Pos. 2,5,8
Seq#:35; Xaa Pos. 4
Seq#:36; Xaa Pos. 4

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34
Seq#:35,36

VERIFICATION SUMMARY   DATE: 02/02/2006
PATENT APPLICATION: US/10/542,867   TIME: 11:41:18

Input Set : E:\401uspc.app.txt
Output Set: N:\CRF4\02022006\J542867:raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:246 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:244
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:398
L:545 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:543
L:695 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:693
L:957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0